AMENDMENTS TO THE DRAWINGS

Please amend Figure 2 by replacing the existing Figure 2 with the Replacement Sheet for Figure 2, which is attached to the end of this paper. An explanation of the changes to Figure 2 are set forth in the Remarks.

REMARKS

THE PROVISIONAL RESTRICTION REQUIREMENT ELECTION

As indicated in the Office Action under reply, a provisional election of claims 1-27 was made on December 18, 2005. With this paper, applicants confirm the provisional election, ***with traverse***.

The method of claims 1-27 and the kit of claims 28-37 both contain the same elements: (1) labeled amplicons; (2) a first differential hybridization probe; (3) a second differential hybridization probe; (4) a first capture probe; and (5) a second capture probe; and means for detecting the signals from the wild-type and variant complexes. The only difference between the method of claims 1-27 and the kit of claims 28-37 is that the capture probes of the kit claims are recited as attached to a substrate. As capture probes are by their very nature attached to a substrate, the recitation of the substrate does not render the two claim sets, i.e., method claims 1-27 and kit claims 28-37, patentably distinct.

Because both sets of claims, i.e., method claims 1-27 and kit claims 28-37, contain the same elements, no burden is imposed upon the Examiner by searching both sets of claims. In light of the foregoing, applicants respectfully request that the Examiner consider claims 1-37 as a set in the instant application.

OBJECTION TO THE SPECIFICATION

The Examiner is objecting to the specification because Figure 2 does not include the assigned SEQ ID NOs as required under 37 C.F.R. § 1.821(d). Attached to this paper is a Replacement Sheet for Figure 2 that amends Figure 2 to include the SEQ ID NOs for the sequences set forth therein. Figure 2 has been further amended to include the sequence listings and SEQ ID NOs for the forward and reverse primers for Exon 1 of CYP2D6, which were not included in original Figure 2. The sequence listings for the forward and reverse primers for Exon 1 are found in the specification as filed at paragraph 83 as SEQ ID NOs 1 and 2.

No new matter has been added to the application with the amendment to the drawings.

AMENDMENT TO THE SPECIFICATION

With the change to Figure 2, paragraph 0023 in the Brief Description of the Drawings has been amended to reflect the sequences set forth in the Replacement Sheet for Figure 2.

Paragraph 0034 has been amended to include the U.S. Patent Application Serial No. of the sister application referenced therein.

In addition to the foregoing, several paragraphs of the specification have been amended to correct a typographical error with respect to the notation for the cytochrome P 450 CY2D6 gene; specifically, in several places of the specification, "CYP2D6" was incorrectly identified as "CPY2D6."

Additionally, as the mark LUMINEX is now a registered trademark, the mark as identified in the application has been amended to reflect that it is now a registered mark with the use of capital letters to identify the mark along with the ® symbol for the federal registration. Other registered trademarks used in the application have also been amended in the same fashion.

No new matter is incorporated into the application with any of the changes made to the specification.

ANTICIPATION REJECTION

Claims 1-27 stand rejected under 35 U.S.C. § 102(b) as anticipated by Beattie et al. This rejection is respectfully traversed.

As recited in claim 1, the present invention relates to a method for detecting the presence or absence of a genetic variation at a polymorphic site in a nucleic acid analyte in a sample comprising contacting *labeled amplicons* from a sample (step a) with a plurality of first and second differential hybridization probes wherein *wild type complexes* are formed between each first differential hybridization probe and a single labeled amplicon having wild type sequences at the polymorphic site, and *variant complexes* are formed between each second differential hybridization probe and a single labeled amplicon having a variant sequence at the polymorphic site (step b). The complexes are detected through hybridization of the complexes to first and second capture probes, wherein a *captured wild type complex* having a first detectable sequence is formed between each wild type complex and a single first capture probe and a *captured variant complex* having a second detectable sequence is formed between each wild type complex and a single second capture probe (steps c and d). The presence or absence of a *genetic variation* in the sample is determined by comparing the relative amounts of the captured wild type and captured variant complexes, wherein a greater amount of captured wild type complexes is indicative of the absence of the genetic variation and a greater amount of captured variant complexes is indicative of the presence of genetic variation (step e).

Beattie et al. teaches a stacking hybridization method for analyzing genomic DNA and expressed sequences using a combination of at least one *stacking probe*, which carries a label (*see*, asterisk in Figures 13-15; col. 15, lines 4-5 and 34-35; and col. 16, line 1 and lines 15-16; col. 19, line 26) and which is not support bound, and at least one *capture probe*, which is support bound (Figures 13-15 and col. 14, lines 54-58). As shown in Figures 13-15, the stacking probes anneal to the target nucleic acid analyte and serve to "place" the position of the capture probe, which in turn interrogates the target sequence (*see also*, col. 14, ll. 54-63). At col. 11, lines 11-33, Beattie et al. explains that the capture probe/stacking probe combination may be used to accurately detect sequence changes at the terminal and adjacent positions on the capture probe and that the stacking probe allows for the screening of sequence changes over a greater

stretch of sequence than the stretches of prior art stacking hybridization assays. Beattie et al. emphasizes that the purpose of the stacking hybridization assay disclosed therein is to increase mismatch discrimination, or in other words to avoid mismatches, by the oligonucleotide probe that is interrogating the sequence (col. 11, lines 16-20, and col. 17, lines 34-37).

Beattie et al. does ***not*** teach or suggest a differential hybridization probe that binds to the capture probe disclosed therein (e.g., claim 1, step b; Figure 3) and also does ***not*** teach or suggest that the stacking hybridization assay disclosed therein uses a comparison of the amounts of captured wild type and captured variant complexes to determine the presence or absence of a genetic variation (e.g., claim 1, step e). As shown in Figure 3 of the instant application and as recited in claim 1, steps b and c, the capture probes of the claimed invention are bound to a solid support and are hybridized to a discrimination probe, which in turn hybridizes to a labeled amplicon. This design is clearly ***not*** analogous to the stacking hybridization assay of Beattie et al., where both the labeled stacking probe and the capture probe bind to the unlabeled target analyte.

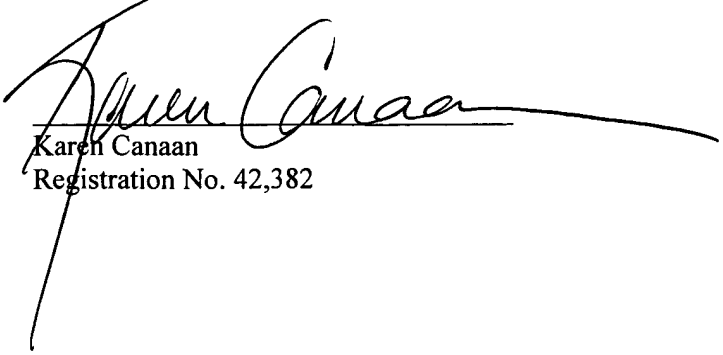
Because Beattie et al. does not teach or suggest the claimed invention, it follows that the claimed invention is not anticipated by Beattie et al. Because the claimed invention is not anticipated by Beattie et al., applicants respectfully request reconsideration and withdrawal of this rejection.

CONCLUSION

With this paper, each of the Examiner's objections and rejections have been fully addressed and overcome. Because there will be no outstanding issues for this application upon entry of this paper, applicants respectfully request withdrawal of all objections and claim rejections and passage of this application to issue.

Any questions regarding this paper or the application in general may be addressed to the undersigned attorney at 650-251-7713 or canaan@reedpatent.com.

Respectfully submitted,

By: 

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